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## REMARKS

Claims 5, 8-12, 15, 17-18, 20-27 and 30-35 are all the claims presently pending in the application. Claim 19 has been canceled. Claims 5, 8-12, 15, 17-18, 20-27 and 30-34 have been amended to more particularly define the invention. Claim 35 has been added.

It is noted that the claim amendments are made only for more particularly pointing out the invention, and <u>not</u> for distinguishing the invention over the prior art, narrowing the claims or for any statutory requirements of patentability. Further, Applicant specifically states that no amendment to any claim herein should be construed as a disclaimer of any interest in or right to an equivalent of any element or feature of the amended claim.

Claim 32 stands rejected under 35 U.S.C. § 112, first paragraph as allegedly not enabled by the specification.

Claims 5, 8-12, 15, 17-27 and 30-34 stand rejected under 35 U.S.C. § 102(b) as being allegedly anticipated by Mendez et al. (Nat. Genet., 1997) as evidenced by Albertson et al. (1990) and the pYAC4 GenBank entry (1995).

Claims 5, 8-12, 15, 17-27 and 30-34 stand rejected under 35 U.S.C. § 101 as being allegedly directed to non-statutory subject matter.

These rejections are respectfully traversed in the following discussion.

## I. THE CLAIMED INVENTION

The claimed invention (e.g., as recited in claim 5, and similarly recited in claims 8, 11, 12 and 15) is directed to a DNA molecule for an organism, the DNA molecule having embedded information, and including a gene portion including a value-added gene which is provided in the gene portion by a source through one of selective breeding, cultivation and gene manipulation, a portion which is other than the gene portion, a watermark including a plurality of nucleotide sequences which are embedded in the portion which is other than the gene portion, and is correlated with source identification information which identifies the source of the value-added gene in the gene portion.

Importantly, a number of nucleotide sequences in the embedded plurality of nucleotide

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sequences is greater than an appearance frequency of the nucleotide sequences which naturally occur in the organism.

Conventional DNA may include a value-added gene embedded therein, in order to improve the characteristics of the organism having the DNA. However, such conventional DNA does <u>not</u> include any information therein to determine the source of the value-added gene embedded therein. Since DNA having such a value-added gene is easily copied, it is difficult to apply technical restrictions to the copying, by third parties, of value-added genes.

The claimed invention, on the other hand, includes a DNA molecule having a plurality of nucleotide sequences which are embedded in a portion of said DNA molecule, a number of nucleotide sequences in the embedded plurality of nucleotide sequences being greater than an appearance frequency of the nucleotide sequences which naturally occur in the organism (Application at Figure 5). These embedded nucleotide sequences may be used to identify the source of genetic information, for example, when the DNA molecule is copied by a third party. Therefore, the claimed invention helps to prevent illegal copying of the value-added gene.

#### Π. THE ALLEGED PRIOR ART REFERENCE

The Examiner alleges that Mendez teaches the claimed invention. Applicant submits, however, that Mendez does not teach or suggest each and every element of the claimed invention.

In particular, Mendez does not teach or suggest "wherein a number of nucleotide sequences in said embedded plurality of nucleotide sequences is greater than an appearance frequency of said nucleotide sequences which naturally occur in said organism", as recited in claims 5 and 12 and similarly recited in claims 8, 11, and 15. As noted above, the embedded nucleotide sequences may be used to identify the source of genetic information, for example, when the DNA molecule is copied by a third party. Therefore, the claimed invention helps to prevent illegal copying of the value-added gene.

Clearly, these features are not taught or suggested by Mendez.

Indeed, the Examiner surprisingly alleges that the "watermark" limitation "can also bet

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literally any DNA sequence that is known to the skilled artisan and is present in the DNA molecule" (Office Action at page 3), and that "the YACs comprised watermark sequences according to the specification" (Office Action at page 4).

However, the Examiner fails to address the fact that in the claimed invention (e.g., claim 1), the watermark includes a plurality of nucleotide sequences which are embedded in the portion which is other than the gene portion. Nowhere does Mendez teach or suggest that the YACs were embedded in a portion of DNA which is other than a gene portion. On the contrary Mendez teaches that the YACs were introduced into mice and he "observed human antibody production" (Mendez at Abstract). Thus, clearly Mendez does not teach or suggest this important feature of the claimed invention.

Moreover, nowhere does the Examiner allege that Mendez teaches a plurality of nucleotide sequences that is correlated with source identification information which identifies the source of the value-added gene in the gene portion.. Indeed, nowhere is this taught or suggested by Mendez.

Further, nowhere does Mendez teach or suggest a DNA molecule having a plurality of nucleotide sequences which are embedded in a portion of said DNA molecule, a number of nucleotide sequences in the embedded plurality of nucleotide sequences being greater than an appearance frequency of the nucleotide sequences which naturally occur in the organism.

Therefore, Applicant submits that Mendez does not teach or suggest each and every feature of the claimed invention. Therefore, the Examiner is respectfully requested to withdraw this rejection.

#### 1III. THE 35 USC 101 REJECTION

The Examiner alleges that the claimed invention is directed to non-statutory subject matter. In particular, the Examiner alleges that the DNA of the claimed invention is not different from that existing in nature.

However, Applicant would point out that the claims have been amended to recite "wherein a number of nucleotide sequences in said embedded plurality of nucleotide sequences

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is greater than an appearance frequency of said nucleotide sequences which naturally occur in said organism" (e.g., claim 1).

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Therefore, the claimed invention is clearly directed to statutory subject matter.

Therefore, the Examiner is respectfully requested to withdraw this rejection.

## IV. FORMAL MATTERS AND CONCLUSION

Applicant notes that claims 5, 8 and 15 and 23 have been amended to address the Examiner's objections thereto.

In view of the foregoing, Applicant submits that claims 5, 8-12 and 15, 17-18, 20-27 and 30-34, all the claims presently pending in the application, are patentably distinct over the prior art of record and are in condition for allowance. The Examiner is respectfully requested to pass the above application to issue at the earliest possible time.

Should the Examiner find the application to be other than in condition for allowance, the Examiner is requested to contact the undersigned at the local telephone number listed below to discuss any other changes deemed necessary in a <u>telephonic or personal interview</u>.

The Commissioner is hereby authorized to charge any deficiency in fees or to credit any overpayment in fees to Assignee's Deposit Account No. 50-0510.

Respectfully Submitted,

Date: 12/9/08

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# CERTIFICATE OF FACSIMILE TRANSMISSION

I hereby certify that the foregoing was filed by facsimile with the United States Patent and

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Trademark Office, Examiner Michael Burkhart, Group Art Unit # 1633 at fax number (571) 273-8300 this \_3 \*\* day of \_\_\_\_\_\_ 2008.

Phillip E. Miller Reg. No. 46,060